

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 19, 2002, 14:50:37 ; Search time 14 Seconds

(without alignments)
1682.754 Million cell updates/sec

Title: US-08-813-323b-2

Perfect score: 3008
Sequence: 1 MESSKKMDSPGALQTNPLK.....IKDDTRFIKIVDTSDLPDP 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match Length | ID | Description |
|------------|--------|---------|--------------|--------------|--------------------|
| 1 | 3008 | 100.0 | 568 | 1 TRA3_HUMAN | Q13114 homo sapien |
| 2 | 2886.5 | 96.0 | 567 | 1 TRA3_MOUSE | Q60803 mus musculu |
| 3 | 837.5 | 27.8 | 501 | 1 TRA2_MOUSE | P39429 mus musculu |
| 4 | 744 | 24.7 | 501 | 1 TRA2_HUMAN | Q12933 homo sapien |
| 5 | 636.5 | 21.2 | 416 | 1 TRA1_HUMAN | Q13077 homo sapien |
| 6 | 628 | 20.9 | 409 | 1 TRA1_MOUSE | P39428 mus musculu |
| 7 | 201 | 6.7 | 438 | 1 DGI7_MOUSE | P11467 dictyostell |
| 8 | 159 | 5.3 | 634 | 1 D147_MOUSE | Q61510 mus musculu |
| 9 | 151.5 | 5.0 | 704 | 1 MEPR_MOUSE | Q61847 mus musculu |
| 10 | 150 | 5.0 | 1005 | 1 RA50_MOUSE | Q58718 methanococ |
| 11 | 149.5 | 5.0 | 919 | 1 RA50_MOUSE | Q58718 methanococ |
| 12 | 148.5 | 4.9 | 1816 | 1 LMA1_MOUSE | P97927 mus musculu |
| 13 | 148 | 4.9 | 1957 | 1 YD86_MOUSE | Q10411 schizosacch |
| 14 | 146.5 | 4.9 | 2230 | 1 GOG4_HUMAN | Q13439 homo sapien |
| 15 | 146 | 4.9 | 1102 | 1 MYSC_CHICK | P29616 gallus gall |
| 16 | 145 | 4.8 | 1679 | 1 YIO9_YEAST | P40457 saccharomyc |
| 17 | 144.5 | 4.8 | 1104 | 1 NEX1_HUMAN | Q12986 homo sapien |
| 18 | 144 | 4.8 | 1727 | 1 ALM1_MOUSE | Q9UK5 schizosacch |
| 19 | 143.5 | 4.8 | 551 | 1 RN27_MOUSE | Q99P12 mus musculu |
| 20 | 143.5 | 4.8 | 852 | 1 RA50_MOUSE | Q9X1X1 thermotoga |
| 21 | 143.5 | 4.8 | 3210 | 1 CENF_HUMAN | P49454 homo sapien |
| 22 | 141 | 4.7 | 879 | 1 RA50_MOUSE | Q58687 pyrococcus |
| 23 | 141 | 4.7 | 1046 | 1 SBCC_MOUSE | Q9CF0 lactococcus |
| 24 | 141 | 4.7 | 1940 | 1 MYH3_MOUSE | P12847 rattus norv |
| 25 | 140.5 | 4.7 | 425 | 1 TM31_MOUSE | Q9B29 homo sapien |
| 26 | 140.5 | 4.7 | 999 | 1 CARE_MOUSE | Q9B29 mus musculu |
| 27 | 140 | 4.7 | 751 | 1 RN27_HUMAN | Q9B29 mus musculu |
| 28 | 139.5 | 4.6 | 794 | 1 HMMR_MOUSE | Q00547 mus musculu |
| 29 | 139 | 4.6 | 390 | 1 TET1_BOVIN | P27628 bos taurus |
| 30 | 138 | 4.6 | 624 | 1 A33_MOUSE | Q02084 pleurodeles |
| 31 | 137.5 | 4.6 | 1607 | 1 MIPR_MOUSE | Q25410 lymnaea sta |
| 32 | 137 | 4.6 | 495 | 1 RA18_HUMAN | Q9NS1 homo sapien |
| 33 | 137 | 4.6 | 886 | 1 RA50_MOUSE | Q29230 archaeglob |

ALIGNMENTS

| RESULT 1 | TRA3_HUMAN | STANDARD: | PRT: | 568 AA. |
|----------------|--|-----------|------|---------|
| ID | Q13114: Q13076: Q13947: Q12990: | | | |
| AC | 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DE | 15-JUN-2002 (Rel. 41, Last annotation update) | | | |
| DE | TNF receptor associated factor 3 (CD40 receptor associated factor 1) | | | |
| DE | (CD40 binding protein) (CD40BP) (LMP1 associated protein) | | | |
| DE | (LAP1) (CAP-1) | | | |
| GN | TRA3 OR CAP1 OR CAP1 | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=95184010; PubMed=7533327; | | | |
| RA | Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D., | | | |
| RT | "Involvement of GRAF1, a relative of TRAF, in CD40 signaling." | | | |
| RL | Science 267:1494-1498(1995). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A., AND CHARACTERIZATION. | | | |
| RC | TISSUE=Lymphoma; | | | |
| RX | MEDLINE=95163092; PubMed=7859281; | | | |
| RA | Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C., | | | |
| RT | Kieff E.; | | | |
| RL | "The Epstein-Barr virus transforming protein LMP1 engages signaling | | | |
| RT | proteins for the tumor necrosis factor receptor family." | | | |
| RL | Cell 80:389-399(1995). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Fetal brain; | | | |
| RX | MEDLINE=95129692; PubMed=7530216; | | | |
| RA | Sato T., Irie S., Reed J.C.; | | | |
| RT | "A novel member of the TRAF family of putative signal transducing | | | |
| RL | proteins binds to the cytosolic domain of CD40." | | | |
| RN | FEBS Lett. 358:113-118(1995). | | | |
| [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=95073988; PubMed=7527023; | | | |
| RA | Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.; | | | |
| RT | "A novel RING finger protein interacts with the cytoplasmic domain of | | | |
| RL | CD40." | | | |
| J. Biol. Chem. | 269:30069-30072(1994). | | | |
| CC | - FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN | | | |
| CC | OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS | | | |
| CC | TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR. | | | |
| CC | - SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR | | | |
| CC | ASSOCIATED FACTORS (POTENTIAL). | | | |
| CC | - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER. | | | |
| CC | - SIMILARITY: CONTAINS 1 MATH/TRAFF DOMAIN. | | | |
| CC | - SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS. | | | |
| CC | ----- | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | | | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | | | |

34 137 4.6 886 1 RA50_MOUSE
35 137 4.6 1938 1 MYH3_HUMAN
36 137 4.6 1940 1 MYH3_HUMAN
37 136.5 4.5 944 1 MYH3_HUMAN
38 136 4.5 704 1 MYH3_HUMAN
39 135.5 4.5 1941 1 MYH3_HUMAN
40 135 4.5 1939 1 MYH3_HUMAN
41 134.5 4.5 1012 1 CX05_HUMAN
42 134 4.5 1940 1 CX05_HUMAN
43 132.5 4.4 630 1 MYH3_CHICK
44 132 4.4 747 1 MYH3_MOUSE
45 132 4.4 1084 1 MYH3_MOUSE

033600 sulfobus
Q9UKX2 homo sapien
P11055 homo sapien
P37380 saccharomyc
P28826 rattus norv
Q9UKX2 homo sapien
P12882 homo sapien
O75665 homo sapien
P02565 gallus gall
O14258 homo sapien
P28825 mus musculu
P02562 oryctolagus

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U21092; AAC50112.1; -
DR EMBL: U19260; AAA65732.1; -
DR EMBL: U138509; AAA68195.1; -
DR EMBL: U15637; AAA6753.1; -
DR Genew; HGNC:12033; TRAF3.
DR MIM; 601896; -
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001293; ZnF-TRAF.
DR InterPro: IPR001841; ZnF-TRAF.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF02176; ZF-TRAF; 2.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR SMART; PS00518; ZF-RING_1; 1.
DR PROSITE; PS00899; ZF-RING_2; 1.
DR PROSITE; PS0145; ZF-TRAF; 2.
DR Zinc-finger; Coiled coil; Repeat.
KW ZN_FING 68 RING-TYPE.
FT ZN_FING 135 190 TRAF-TYPE 1.
FT ZN_FING 191 249 TRAF-TYPE 2.
FT DOMAIN 267 338 COILED COIL (POTENTIAL).
FT DOMAIN 418 503 MATH/TRAF.
FT CONFLICT 129 129 T->M (IN REF. 2 AND 4).
FT CONFLICT 134 134 MISSING (IN REF. 4).
FT CONFLICT 218 242 MISSING (IN REF. 3).
FT CONFLICT 339 339 P->S (IN REF. 3).
FT CONFLICT 405 405 R->G (IN REF. 4).
SQ SEQUENCE 568 AA; 64460 MW; 6765533FBE523C88 CRC64;

Query Match 100.0%; Score 3008; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 9.2e-173;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSKMDSPGALQTPPLKTHDRSAGTPVPVPEGGYKKEKFKVTEYKKECEKCHVL 60
DB 1 MESSKMDSPGALQTPPLKTHDRSAGTPVPVPEGGYKKEKFKVTEYKKECEKCHVL 60
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFVFNCCCKREIILQTYCRNE 120
DB 61 CSPKQTECHRCESCMALLSSSPKCTACQESIYKDKVFVFNCCCKREIILQTYCRNE 120
QY 121 SRGCAQLTLGLHLVHLKNDCHFEELPCVRPCKEYKVRKLDIHDYKACKYREATCSHC 180
DB 121 SRGCAQLTLGLHLVHLKNDCHFEELPCVRPCKEYKVRKLDIHDYKACKYREATCSHC 180
QY 181 KSOVPALALOKHEDTDCPCVVVSCPHKCSVOTLLNSELSAHLSECVNAPSTCSFRYGV 240
DB 181 KSOVPALALOKHEDTDCPCVVVSCPHKCSVOTLLNSELSAHLSECVNAPSTCSFRYGV 240
QY 241 POGTNOQIKAHFASSAVQHVNLKEMNSLEKRVSLQNESYEKKKSIOSLNQICSEFI 300
DB 241 POGTNOQIKAHFASSAVQHVNLKEMNSLEKRVSLQNESYEKKKSIOSLNQICSEFI 300
QY 301 EIERQKEMLRNNEKSLIHLQRIYDSQAEKLELKEIRFRONWBEADSMKSSVSLONR 360
DB 301 EIERQKEMLRNNEKSLIHLQRIYDSQAEKLELKEIRFRONWBEADSMKSSVSLONR 360
QY 361 VTELEVSVDKASGVANRTGLLESQLSRHHOMLSVHDIRLADMDLRFQVLETASYNGVLI 420
DB 361 VTELEVSVDKASGVANRTGLLESQLSRHHOMLSVHDIRLADMDLRFQVLETASYNGVLI 420
QY 421 KTRDYKRRKQZAVMGKTLISLYSQPFYTGFGYKMCARVYLNDGKGKTHLSLFFVIMRG 480
DB 421 KTRDYKRRKQZAVMGKTLISLYSQPFYTGFGYKMCARVYLNDGKGKTHLSLFFVIMRG 480

QY 481 EYDALLPWPFKOKYVTLMLMDGSSRRHLGDAFKPPDNSSPKKPTGEMNIASGCPVFAQ 540
DB 481 EYDALLPWPFKOKYVTLMLMDGSSRRHLGDAFKPPDNSSPKKPTGEMNIASGCPVFAQ 540
QY 541 TVLENGTYIKDDTIFIKVIVDTSLLPDP 568
DB 541 TVLENGTYIKDDTIFIKVIVDTSLLPDP 568

RESULT 2

TRAF3_MOUSE STANDARD; PRT; 567 AA.
AC 060803; 062380;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
DE (CRAFT) (TRAFAMN).
GN TRAF3 OR CRAFT OR TRAFAMN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAFT, a relative of TRAF, in CD40 signalling.";
RL Science 267:1494-1498(1995).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
RA Dinulos M.B., Distcheve C.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lacy E.;
RT "A candidate gene for the amniotless gastrulation stage mouse mutation
RT encodes a TRAF-related protein.";
RL Dev. Biol. 177:274-290(1996).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
CC TO CD40 AND THE LYMPHOTOKIN-BETA RECEPTOR (BY SIMILARITY).
CC SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
CC ASSOCIATED FACTORS (POTENTIAL).
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
CC FOUND IN LIVER.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U21050; AAC52175.1; -
DR EMBL: U33840; AAC52710.1; -
DR MGD; MGI:108041; Traf3.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001293; ZnF-TRAF.
DR InterPro: IPR001841; ZnF-TRAF.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF02176; ZF-TRAF; 2.
DR SMART; SM00061; MATH; 1.

DR SMART: SM00184; RING: 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROSITE: PS50145; ZF_TRAF; 2.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 67 76 RING-TYPE.
 FT ZN_FING 134 189 TRAF-TYPE 1.
 FT ZN_FING 190 248 TRAF-TYPE 2.
 FT ZN_FING 266 337 COILED COIL (POTENTIAL).
 FT DOMAIN 417 502 MATH/TRAF.
 FT CONFLICT 72 73 CE -> MQ (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 FT SEQUENCE 567 AA; 64263 MW; 25228343B41192DC CRC64;
 Query Match 96.08; Score 2886.5; DB 1; Length 567;
 Best Local Similarity 96.18; Pred. No. 1,7e-165;
 Matches 546; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

OY 1 MESSKKMSPGALQTNPLKLTDRSAGTPVPEQGGYKKEFKVTKEDKCKEHLVL 60
 DB 1 MESSKKMSPGALQTNPLKLTDRSAGTPVPEQGGYKKEFKVTKEDKCKEHLVL 59
 OY 61 CSPKTECGHRCESCMALLSSSSPKCTACQESIIVKDKVCKCKREILALQYCRNE 120
 DB 60 CNPKTECGHRCESCMALLSSSSPKCTACQESIIVKDKVCKCKREILALQYCRNE 119
 OY 121 SRGCAEQLTLGHLVNLKNDCHFEELPCVPRDCKEYLRKLRDHYEACKYREATCSHC 180
 DB 120 GNGCAEQLTLGHLVNLKNDCHFEELPCVPRDCKEYLRKLRDHYEACKYREATCSHC 179
 OY 181 KSOVMNLQKHEDTDCPCVYVSCPHKCSVOTLSELSAHLSECVNAPSCSKRYGCY 240
 DB 180 KSOVMNLQKHEDTDCPCVYVSCPHKCSVOTLSELSAHLSECVNAPSCSKRYGCY 239
 OY 241 FQGTNOQIKAHBSAVOHVNLKEMSNLEKRVSLQNESVEKNKSIOSLHNOCSFEI 300
 DB 240 FQGTNOQIKAHBSAVOHVNLKEMSNLEKRVSLQNESVEKNKSIOSLHNOCSFEI 299
 OY 301 EIERKEMLRNNESKILHQRVIDSQAEKLEKEIRPFQNMFEADSMSSVESLONR 360
 DB 300 EIERKEMLRNNESKILHQRVIDSQAEKLEKEIRPFQNMFEADSMSSVESLONR 359
 OY 361 VTELSVDKSAQOVARNTGLESQLSRHDOMLVHDIRLADMDLRFQVLETAHYGVLIW 420
 DB 360 VTELSVDKSAQOVARNTGLESQLSRHDOMLVHDIRLADMDLRFQVLETAHYGVLIW 419
 OY 421 KIRDYKRRKQEAVMGKTLISYQPEYTGFGYKMCARVYLANGDGKGTSLLEFVIMRG 480
 DB 420 KIRDYKRRKQEAVMGKTLISYQPEYTGFGYKMCARVYLANGDGKGTSLLEFVIMRG 479
 OY 481 EYDALLPWFKQKVTLMDDGSSRRHIGDAKPPNNSSPFKPTGEMNINISGCPVFAVQ 540
 DB 480 EYDALLPWFKQKVTLMDDGSSRRHIGDAKPPNNSSPFKPTGEMNINISGCPVFAVQ 539
 OY 541 TVLENGTYIKDDTIFIKVIVTSDLPDP 568
 DB 540 TVLENGTYIKDDTIFIKVIVTSDLPDP 567

RESULT 3
 TRAF_MOUSE
 ID TRAF_MOUSE STANDARD: PRT: 501 AA.
 AC P39429:
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE TNF receptor associated factor 2 (TRAF2).
 GN TRAF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-94349371; PubMed-8069916;
 RA Rott M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor";
 RL Cell 78:681-692(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
 CC ACTIVATES NF-KAPPA-B.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
 CC HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
 CC PROTEIN 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
 CC FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL: I35303; AAC37662.1; -
 CC HSSP: P12351; 1HMT.
 CC WGI: MG1101835; TRAF2.
 CC InterPro: IPR002083; MATH.
 CC InterPro: IPR003007; TRAF.
 CC InterPro: IPR001293; Znf_TRAF.
 CC InterPro: IPR001841; Znf_fing.
 CC Pfam: PF00097; Zf-C3HC4.1.
 CC Pfam: PF00917; MATH; 1.
 CC Pfam: PF02176; Zf-TRAF; 2.
 CC SMART: SM00184; RING; 1.
 CC SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROSITE: PS50145; ZF_TRAF; 2.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 34 73 RING-TYPE.
 FT ZN_FING 124 180 TRAF-TYPE 1.
 FT ZN_FING 177 233 TRAF-TYPE 2.
 FT DOMAIN 298 348 COILED COIL (POTENTIAL).
 FT DOMAIN 334 501 MATH/TRAF.
 FT SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;
 Query Match 27.88; Score 837.5; DB 1; Length 501;
 Best Local Similarity 33.68; Pred. No. 3.5e-43;
 Matches 196; Conservative 89; Mismatches 194; Indels 105; Gaps 17;

OY 3 SSKRMDSFGALQTNPLKLTDRSAGTPVPEQGGYKKEFKVKT-VEDKYCKEHLVL 61
 DB 2 AAASVTSPGSELELQ-----GSKTLGTRLEAKYCSACKNILR 42
 OY 62 SPKTECGHRCESCMALLSSSSPKCTAC-----QESI---VKQVFFDNCKKREILA 112
 DB 43 RPFQAGCHRYCSFCLTSLSSGPNCAACVBYEGISLESSAFPDNARRVES 102
 OY 113 LQIYCRNRCGABQLTLGHLVNLKNDCHFEELPCVPRDCKEYLRKLRDHYEACKY 172
 DB 103 LPAYCPND--GCTWKGTLKEYESCHGELCPFLTEC--PACKGLVLRSEKHNHTEGCPK 158
 OY 173 REATCSHCKSOVPMIALQKHEDTDCPCVYVSCPHKCSVOTLSELSAHLSECVNAPSC 232
 DB 159 RSLSCCHRCAPCSHVVDLVEHYEV--CPKPEPLTG--DGCKKKIIPREFQDHYRACSKRYLC 216
 OY 233 SFKRYGCVFQGTNOQIKAHBSAVOHVNLKEMSNLEKRV-----LQNESV 282
 DB 217 RFTVYGCSENVETENLDHQLREHLALL--LSTLEADASGTGLNVOYGPDLQNCQI 274

DE TNF receptor associated factor 1 (TRAF1) (Epstein-Barr virus-induced protein 6).

DE TRAF1 OR EB16.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoma;

RX MEDLINE=95163092; PubMed=7859281;

RA Mosialos G., Birkenbach M., Yalanchilli R., Vanarsdale T., Ware C., Kleef E.;

RA "The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.";

RT Cell 80:389-399(1995).

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).

CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

CC EMBL: U19261; AAA62309.1; -

CC DR Genev; HGNC:12031; TRAF1.

CC DR MIM: 601711; -

CC DR InterPro: IPR002083; MATH.

CC DR InterPro: IPR003007; TRAF.

CC DR Pfam: PF00917; MATH; 1.

CC DR SMART: SM00061; MATH; 1.

CC KW Coiled coil.

CC FT DOMAIN 182 264 COILED COIL (POTENTIAL).

CC FT DOMAIN 269 354 MATH/TRAF.

CC FT SEQUENCE 416 AA; 46163 MW; A956A123AA0D284A CRC64;

CC SQ

Query Match 21.2%; Score 636.5; DB 1; Length 416;

Best Local Similarity 35.3%; Pred. No. 2,9e-31;

Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

DB 138 KNOCHHELPVCPRDCKEVLKRDLDHVEKACKYREATCSHCKSQVPMIALQKHEDTDC 197

DB 15 ENEPRECPPTVCODPREP-----RATCCAGCLSNP-----RNGEDQIC 54

QY 198 PCVAVSCPHKCSYQTL-----LNSLSAHLSECVNAPSTCSFKRGVCGTNOQIK 249

DB 55 P-----KCRGEDIQISPGSRLRTOEKAN-PEVAEAGIGCPFAGVGSQSQSVQ 105

QY 250 AHEASSAVQVNL-----KEMS-----NSLEKVSLLQ-NESEVKNKSIO-SLH 292

DB 106 EHEVTSQTHNLGLGFMKQMKARLGGLESPMALEQNLSDLOAAVEVADDEVDCC 165

QY 293 NQICSPFEIEROKEMLRNNSKILHLQRYIDSOAEKLELDEIRFERNWEDADSMKS 352

DB 166 RAPS-----ESQEE-----LALQHPM--KEKLLALEGLRVF-----E 198

QY 353 SVESLQNVLELVSDKAGVANTGLLSQLSRH-----DQMLSVHDIRLA 400

DB 199 NIVAVLNKEVE-----ASHIALATSIHOSQIDREIRILSEORVVELQDTLQKQDALG 251

QY 401 DMDLRFOVLETSYNGVLIKIRDKRRKQEAQVNGKTLISYQPFYTGEGYKMCARVYL 460

DB 252 KLEOSLRIMEASFDGFLMKITVTRRCHESACGRIVSLSPAFYTAQKGYKLCALTYL 311

QY 461 NGDGMKGTHLSLFYIMNGEYDALLPMPFKOKVTLMIMDQSSRRHLGDAFKPPNNS 520

DB 312 NGDGTCKRTHLSLFYIMNGEYDALLPMPFRKRVFEMLDQ--NNREHALDARPLSSAS 370

QY 521 FKKPTGEMNIASCPVEVAQVLEN--GTIYIDDTIFITVIYDTS 563

DB 371 FQRPSQETVNASCPLEFPLSKLQSPKHAHYVDDIMFLKCIQVETS 415

RESULT 6

TRAF1_MOUSE STANDARD; PRT; 409 AA.

AC P39428;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TNF receptor associated factor 1 (TRAF1).

GN TRAF1.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.

RX MEDLINE=94349371; PubMed=8065916;

RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;

RT "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

RL Cell 78:681-692(1994).

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). THIS HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

CC EMBL: L35302; AAC37663.1; -

CC DR MGD: MGI:101836; Traf1.

CC DR InterPro: IPR002083; MATH.

CC DR InterPro: IPR003007; TRAF.

CC DR Pfam: PF00917; MATH; 1.

CC DR SMART: SM00061; MATH; 1.

CC KW Coiled coil.

CC FT DOMAIN 167 256 COILED COIL (POTENTIAL).

CC FT DOMAIN 262 347 MATH/TRAF.

CC FT SEQUENCE 409 AA; 45464 MW; EBA7FEE539FEDDF CRC64;

CC SQ

Query Match 20.9%; Score 628; DB 1; Length 409;

Best Local Similarity 36.6%; Pred. No. 9e-31;

Matches 154; Conservative 69; Mismatches 128; Indels 70; Gaps 13;

DB 173 REATCSHCKSQVPMIALQKHEDTDCPCVAVSCPHKCSYQTLRLSELASHLSECVNAPSTC 232

DB 28 RVLCCTACASE-----NLNRDEDRICPKCADMLHVPSPSLTQF-KVN-SQVAEALMC 81

QY 233 SFKRGVCGTNOQIKAEASSAVQVNL-----LKEMS-----LEKVSLL 277

DB 82 PFAGVGSCKSPQSQVQHEATQSOSHLVLLAVLKEMSSPGSNGSPMALENNLSEL 141

QY 278 QNESEVKNKSISQSLNQICSPFEIEROKEMLRNNSKILHLQRYIDSOAEK-LKELDKE 336

DB 142 Q-----LQAAVATGDLVDVCRAPCCSQEELALQHLVK-----EKLQLODEK 186

QY 337 IRPFROMWEADSMKSSVESLQNRVTELSVDKAGOVARNITGLSELSRH----- 388
 Db 187 LRVF-----ANIVAVLNKEVE-----ASHLLALASINHSQDLREHLLSEOR 228
 QY 389 -----DQMLSVHDIRLADMDLRFQVLETAHYNGVLLWKIDYKRRKQEAVMGKTLISYOP 444
 Db 229 VVELQOTLQKQDVGLKLEHSLRLMEASFDGTFELMKITNVTRKCHESVCGRVSLFSPA 288
 QY 445 FYTGYGFKKCAVYLNQGMGKGTLSLFEVIMRGEVYALLPMPKQKVTLMINDQSS 504
 Db 289 FYTAKYGYLCLRLYLNQSGSKKTLSTFIYIMGEYDALLPMPKRNKVTMLDQ--NN 347
 QY 505 RRLHGAEPDPNSSFKKPTGEMNIAAGCPVFAQVLEN--GTYIKDDTFIRIYVDE 562
 Db 348 REHALIDAFRDLSSASFQROSETNVAAGCPLEFPLSKLQSPKHAIVYDDTFELKCIYDT 407
 QY 563 S 563
 Db 408 S 408

RESULT 7

Db17_DICDI STANDARD: PRT: 458 AA.
 AC P11467, 1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DG17 protein.
 GN ZFAA OR DG17.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 OX NCBI_TaxID=44689;
 RN [1]
 RX MEDLINE=88142840; PubMed=2830496;
 RA DISCOLL D.M., Williams J.G.;
 RT "Two divergently transcribed genes of Dictyostelium discoideum are cyclic AMP-inducible and coregulated during development.";
 RL Mol. Cell. Biol. 7:4482-4489(1987).
 CC -1- INDUCTION: BY CAMP DURING AGGREGATION.
 CC -1- MISCELLANEOUS: THE EXPRESSION OF DG17 PROTEIN IS DEVELOPMENTALLY REGULATED.
 CC -1- SIMILARITY: CONTAINS 1 TRAF-TYPE ZINC FINGER.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M18106; AAA3192.1; -
 DR PIR: A29361; A29361.
 DR DictyDb: DD02010; zfaa.
 DR InterPro: IPR002083; MAT.
 DR InterPro: IPR001293; Zn1-TRAF.
 DR InterPro: IPR001841; Zn1_finger.
 DR Pfam: PF00917; MAT; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MAT; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: PS00145; zf-TRAF; 1.
 DR PROSITE: PS00145; zf-TRAF; 1.
 KW Developmental protein; zinc-finger.
 FT SIMILAR 25 67 TO DROSOPHILA SINA (AA 71-108).
 FT ZN_FING 27 66 POTENTIAL.
 FT ZN_FING 193 250 TRAF-TYPE.
 SO SEQUENCE 458 AA; 53015 MW; FE4804D9AB90EB26 CRC64;

Query Match 6.7%; Score 201; DB 1; Length 458;
 Best Local Similarity 20.1%; Pred. No. 3.3e-05;
 Matches 115; Conservative 77; Mismatches 174; Indels 206; Gaps 28;

QY 48 EDKYCEKCHLVLPKOTEC--GHFCESCMAALLSSSPKCYACO-----ESI 95
 Db 22 NKRYCPICFEIYKQIYQCKSGHHACKCEKWEKSLFKK-ECMTCKSYVNSYNDLSRL 80
 QY 96 VKDYF--KDNCC--KRELLAQIYC-----RNSRGAEDLTIGHL 134
 Db 81 MVERAFDKKECCCIYSFNEQIVEGTNCSPPDGASVONORNLIDENNGCKEKIEVDID 140
 QY 135 VHLKNDCHFEELPCVRPDKKELVRLKDLRDHVEKACYREATCSHK--SOVPMIALQKH 193
 Db 141 SHLIN--QCKRVYTSFNGC--EKILR--MNSIKNGGFKLVTDPCFKRDIIKKLETHY 195
 QY 194 DTDCPCVAVSCPHGCVQTLRLSELSAHLECVNAPSTCSFKRYGVQGTNOOIKRHEA 253
 Db 196 KT--CPVPIDCSQGCSYKIEKRSIIDHIENDCQNTQIPCKYFEGC-----240
 QY 254 SSAVOHNLKEMNSLEKRVYSLQNESVEKNSIOSLHQISFLEIRQKEMLRNNE 313
 Db 241 -----KVMKRSSELQ----- 251
 QY 314 SKILHQRVIDSQAEKLEKELDKETIRPFROMWEADSMKSSVESLQNRVTELSVDKAG 373
 Db 252 -----HLERV-----NHQNY-----MGLIEKLTQV-----GQ 275
 QY 374 VARTGLESQLSRHDM-----LSYHDIRLADMDLRFQVLETA--SYNGVL-TMKIR 423
 Db 276 SKRT-----HDELLKRIEDLSLVYKFDACIKQVLEKALDICSNGYRNKWIIS 325
 QY 424 DY-----KRRKQEAVMGKTLSTYQPFYGYFYKMCARVYLNQGMGKGTLSLFEVY- 477
 Db 326 NYSVAKSKINCAALSPMISLISHF-----QVC--VYKGD--ENKEYSILYLRN 374
 QY 478 -----MRGEYDALLPMPKQKVTLMINDQSSRHLGDAKPDENSSFFKPTGEMNI 530
 Db 375 NIEPNSLAKVEYSFTL-----VNVLDKKSIRKKD-----KKRVFISE 414
 QY 531 ASGCPVFAQVTL--ENGTYIKDDTFIRIYIV 560
 Db 415 GWGWRFLSLDLINKENGLSNDKLITBIYI 446

RESULT 8

Db17_MOUSE STANDARD: PRT: 634 AA.
 AC 061510, 2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE zinc finger protein 147 (Tripartite motif protein 25) (Estrogen responsive zinc finger protein) (Efp).
 GN ZNF147 OR TRIM25 OR ZFP147 OR EFP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=96025835; PubMed=7592654;
 RA Orlino A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
 RT "Molecular cloning, structure, and expression of mouse estrogen-responsive zinc finger protein Efp. Co-localization with estrogen receptor mRNA in target organs.";
 RL J. Biol. Chem. 270:24406-24413(1995).
 CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL, D63902; BAA09941.1; -

DR MGD; MG1:102749; Trlms25.

DR InterPro: IPR001870; Gamma_carboxylase.

DR InterPro: IPR003878; SPRY_domain.

DR InterPro: IPR003877; SPRY_receptor.

DR InterPro: IPR001841; znf.fing.

DR Pfam; PF00067; zf-C3HC4; 1.

DR Pfam; PF00622; SPRY; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00449; SPRY; 1.

DR PROSITE; PS00518; ZF_RING_1; 1.

DR PROSITE; PS00589; ZF_RING_2; 1.

DR Zinc-finger; Coiled coll.

KW ZN_FING 13 54 RING-TYPE.

FT ZN_FING 13 54 COILED COLL (POTENTIAL).

FT DOMAIN 215 305 SPRY.

FT DOMAIN 514 631 SPRY.

SC SEQUENCE 634 AA; 71772 MW; 66959DE2832E611 CRC64;

Query Match 5.3%; Score 159; DB 1; Length 634;

Best Local Similarity 18.7%; Pred. No. 0.015;

Matches 75; Conservative 69; Mismatches 130; Indels 128; Gaps 17;

OY 49 DKYKCEKHLVLCSPKQTEGHCRCESMAALLSSSP--KCTACQEST-VKDKVFKN- 104

DB 9 EELSCVCLLEFKRPVTPCGHNECTSLDETWWVGPRYPKPCRCRYGVAPOLAKNTV 68

OY 105 -CCKRE-----ILALQIVRNBSRGCAEOLTLGHLVHKN 139

DB 69 MCAVVEQELQAOARTPVDDWTPRRFSSASNAIVACDH---CLTEIAKTLCLVCMAS 124

OY 140 DC-----HFEELPCVRPCKEKVLKDLRDHVERAK--KYRATCSHCKSGVPMIAL 189

DB 125 FQGHILRPFFDS-----PAFQDHPLOSPIRDLRRKCTQHNLRBFECF- 168

OY 190 QAHEDTDCCVVSCPRK-CSVOTLLRSLSHLSGCVNAPSTCSFKRYGCGVFOGTNOI 248

DB 169 ---EHGECICICLVHKKCSPTTL--SQASADL----- 197

OY 249 KAHESAVOHNLKEMSNLEKRVSLQNSVEKNKSIOSLHNOICSEIEIEROKEM 308

DB 198 -----EYKLRNKLITLHSHINATKALEVRSKQCVQDSMKRMKQ 239

OY 309 LRNNESKILHLOKVID---SQAELKELDKEI-----RPFQNMFEADSMKSVES 356

DB 240 LR---OEYEMKAVIDAETSSLRLRLEKEKRYGKFTDIYGVLVKKSEMOKLAEVEL 296

OY 357 LONRVTELESVDKSA---GOVARNTGLLSQLSRHDQMLSVH 395

DB 297 IMDKGEFEFLKAKALQGESIKRYVIPIRIDDL-HLLINGIV 337

RESULT 9

MEPB_MOUSE STANDARD: PRT: 704 AA.

AC 061847;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2).

GN MPR18 OR MEP-18.

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP [1]

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Kidney;

RA MEDLINE=94012651; PubMed=8407940;

RA Gorbee C.M., Marchand P., Jiang W., Copeland N.G., Gildert D.J.,

RA Jenkins N.A., Bond J.S.;

RT "Cloning, expression, and chromosomal localization of the mouse

RT Meprin beta subunit.";

RL J. Biol. Chem. 268:21035-21043(1993).

RN (2)

RN SEQUENCE FROM N.A. (ISOFORM BETA').

RC TISSUE=Kidney;

RX MEDLINE=96147211; PubMed=8567689;

RA Dietrich J.M., Bond J.S., Jiang W.,

RT "A novel meprin beta mRNA in mouse embryonal and human colon

RT carcinoma cells.";

RL J. Biol. Chem. 271:2271-2278(1996).

CC -1 CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates

CC preferentially on carboxyl side of hydrophobic residues.

CC -1 COPFACTOR: BINDS 1 ZINC ION.

CC -1 SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH

CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED

CC HETERODIMERS.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein.

CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS, THE BETA AND BETA' SUBUNITS, AND

CC DIFFER IN THEIR N-TERMINUS DUE TO DIFFERENTIAL PROMOTER USAGE AND

CC ALTERNATIVE SPLICING.

CC -1 TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY,

CC INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM

CC HAS BEEN FOUND IN CARCINOMA CELLS.

CC -1 INDUCTION: By retinoic acid.

CC -1 PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS

CC ARE GLYCOSYLATED.

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

CC -1 SIMILARITY: CONTAINS 1 MAM DOMAIN.

CC -1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC at the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: L15193; AAA75234.1; -

DR HSRP; P28825; IIAF.

DR MEROPS; M12.004; --1b.

DR MGD; MG1:96964; Mep1b.

DR InterPro: IPR001506; Astacin.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000998; MAM_domain.

DR InterPro: IPR002083; MATH.

DR InterPro: IPR003007; TRAF.

DR InterPro: IPR000130; Zn_mtpeptidse.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00629; MAM; 1.

DR Pfam; PF00917; MATH; 1.

DR Pfam; PF01400; Astacin; 1.

DR PRINTS; PR00480; ASTACIN.

DR PRINTS; PR00020; MAMDOMAIN.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00137; MAM; 1.

DR SMART; SM00661; MATH; 1.

DR SMART; SM00235; znmc; 1.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

DR PROSITE; PS00740; MAM_1; 1.

DR PROSITE; PS00600; MAM_2; 1.

DR PROSITE; PS00022; EGF_1; FALSE_NG.

DR PROSITE; PS01186; EGF_2; FALSE_NG.

KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Glycoprotein;

KW Zymogen; Signal; EGF-like domain; Alternative splicing.

FT SIGNAL 1 20

FT PROPEP 21 64

FT CHAIN 65 704

FT DOMAIN 21 654

FT TRANSMEM 655 678

FT DOMAIN 679 704

BY SIMILARITY.

MEPRIIN A BETA-SUBUNIT.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

```

FT DOMAIN 63 260 METALLOPROTEASE.
FT DOMAIN 601 430 MAM.
FT DOMAIN 607 647 EGF-LIKE.
FT METAL 153 153 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 154 154 BY SIMILARITY.
FT METAL 157 157 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 163 163 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 611 622 BY SIMILARITY.
FT DISULFID 616 631 BY SIMILARITY.
FT DISULFID 633 646 BY SIMILARITY.
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 27 MDARQPMFVFAFATLILASGLPADEKF -> MNSTAGPASR
SRHSFKRCMKILKAPRDGMVMTFG (IN ISOBOM
BETA').
SQ SEQUENCE 704 AA; 79548 MW; 2D6105DD74650F70 CRC64;

Query Match 5.0%; Score 151.5; DB 1; Length 704;
Best Local Similarity 25.1%; Pred. No. 0.049;
Matches 54; Conservative 38; Mismatches 56; Indels 67; Gaps 11;

OY 392 LSVHDIRLMDLRFOVETASTYNGVLIMKIDYRKROEAVMGKTLISYSPFTGTGFG 451
DB 416 LSIIDININSETGCPHH-----IWHIONF-----TOLIGODITVSPPFYSSK-G 459
OY 452 YKMCARVYLINGDGKMGKTHLSLEFVIMRGEYDALLPWPFK-QKXTLMDQ----- 501
DB 460 YAF-QIYMD--LRYSTNVGIYFHLISGANDDQLQMPQOQATMTLLDQNPDIRQME 514
OY 502 -----GS-----SRRLGDAFKPDNPSSSRKPKGEMNIAISGCPVPAQ 540
DB 515 NORSTTPPTMTSDNGSTFWDRPSKVGVTDF--PNGTQFSR-----GIGYGTTFITR 566
OY 541 TVLENGYIKDDTIFIKYIVD-----TSDLPDP 568
DB 567 ERLKREFTKGDYIYLLTVEDISHLNSTSAVPP 601

RESULT 10
RA50_METUA STANDARD; PRT; 1005 AA.
ID RA50_METUA
AC Q58718;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR MJ1322.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
ON NCBI_TaxID=2190;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA MEDLINE=96337999; PubMed=8688087;
RA Sultun G.G., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Kelavage A.R., Dougherty B.A., Tomb J.F., Adams R.A., Gocayne J.D.,
RA Overbeek R., Kirkness E.F., Weisdom K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RA Science 273:1058-1073(1996).

```

```

CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of exonuclease unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U67572; AAB99331.1; -.
CC TIGR; MJ1322; -.
CC DR InterPro: IPR003439; ABC_transport.
CC DR InterPro: IPR003405; SMC_C.
CC DR InterPro: IPR003395; SMC_N.
CC DR Pfam; PF02463; SMC_N; 1.
CC DR Pfam; PF02483; SMC_C; 1.
CC DR Prodom; PD000006; ABC_transport; 1.
CC KW DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
CC NP_BIND 32 39
CC FT DOMAIN 158 849 COILED COIL (POTENTIAL).
CC SEQUENCE 1005 AA; 119387 MW; 9BBB48173E78B8F3 CRC64;

Query Match 5.0%; Score 150; DB 1; Length 1005;
Best Local Similarity 19.8%; Pred. No. 0.09;
Matches 73; Conservative 77; Mismatches 102; Indels 116; Gaps 18;

OY 130 LGHLVHLKNDGFEELPCVPRDCKEYVLRKIDRHYEAKCKRTGCHSGQVPMAL 189
DB 346 LDTLLNKKIKOE--IERETIK-DLLEL--KNINEIEKIEYKR-ICECKEY----- 393
OY 190 QKHEDTDCPCVVVSPCHKSVOTLNLSELSAHLSECVNAPSTCSFRYCGVGTNOQIK 249
DB 394 -----YKLT-----LELEK 403
OY 250 AHEASS-AVOHVLKEMSNLSLEKVSLO--NESVE--KNKSIOSLNOJCFEIELE 303
DB 404 AVEYNKLTLEYITLQOE-KKSEIKININDETRINKLEETKNDISIENSL-----KEIE 458
OY 304 ROKEMLRNNSKTLIHOR--VIDSAEKIKELDEIR-----PFRQNMEDAS 349
DB 459 EKKKVLLENLOKEKTELEKKEINSEIKRUKITLDELKEVEGCKPLCKTPIDEN-KKML 517
OY 350 MKSSVSLQNRVELESVDKSAQAVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVL 409
DB 518 INGHKTQNLNKKYELKEIKKIREIKDEIKKEIKDEIKENIKT-----LKTLYL 567
OY 410 ETASVNGVLIWKTRDYKRRKQEAVMGKTLISL--SQP-----YTSYFGYK 453
DB 568 EKSOQIEELDELKLNKYEQDLDE--INKKISVYVNGKPVDELIEDIKSQLNKKFNFYNOY 625
OY 454 MCARYLYN 461
DB 626 LSAVSYLN 633

RESULT 11
RA50_AERPE STANDARD; PRT; 919 AA.
ID RA50_AERPE
AC Q9YFZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR APE0110.
OS Aeropyrum pernix.

```


Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 CC Desulfurococcales; Aeropyrum.
 CC NCBI_TaxID=56636;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jino K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamaya M., Maeda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
 CC rad50/mre11 complex possesses single-strand endonuclease activity
 CC and ATP-dependent double-strand-specific exonuclease activity.
 CC Rad50 provides an ATP-dependent control of mre11 by unwinding
 CC and/or repositioning DNA ends into the mre11 active site (By
 CC similarity).
 CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY RAD50 SUBFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC
 CC EMBL: AP000058; BAA79020.1;
 DR InterPro: IPR003439; ABC_transportr.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N.1.
 DR Pfam: PF02483; SMC_C.1.
 DR DNA_repair; Hydrolyase; ATP-binding; Coiled coil; Complete proteome.
 DR NP_BIND 31 38 ATP (By similarity).
 FT DOMAIN 202 758 COILED COIL (POTENTIAL).
 FT SEQUENCE 919 AA: 104138 MW: 784480EB601B9DD CRC64;
 SQ
 Query Match 5.0%; Score 149.5; DB 1; Length 919;
 Best Local Similarity 21.1%; Pred. No. 0.087;
 Matches 90; Conservative 63; Mismatches 157; Indels 117; Gaps 15;
 Oy 61 CSKRCGHRCEGSMALLSSSPKCAQESYKDKVFQDNCKREILALQYCR-- 118
 Db 402 CRRKDL-CGSEKPEVLERL-----DAVINLESARALDQASLLEARRL 448
 Oy 119 -----NSRGCAEQLTGLHLVHLKNDCHFEELPCVPDCKEYLRKLDHVEKACK 171
 Db 449 VQALSMLESGSGARCPVG-----AELPPGAAEIAIRYRHE-AERLRKA 495
 Oy 172 YREATSCHCKSOVPATLAKHEDTDCPCVAVSCPRKCSQVTLR--SELSAHLSECVNAP 229
 Db 496 EKAAEEKARAEASRLQDKRR-----TELLSRLNQLDEGLRE----- 534
 Oy 230 STGCFRRCYGVFGCTNOQKAHEASSAV-OHVNLKEMNSLEKKVSLQNESV---EK 284
 Db 535 -----LGFQTPEDLAKAEKQLMLRERLEFKLNSLEKFRNLSREVALREAK 585
 Oy 285 NKSISLHNOICFSEIEROKEMLNNSKILHLQRTVDSQAEKL----- 330
 Db 586 TRALEVLQR---LGIKKEPARREKLTLSSEKRLERMLVSKEDLATRLGITYARSLD 641
 Oy 331 -----KEL---DKETPRPROMHEEDSKSSVESIQNVTELESVDKAGV 374
 Db 642 LLEKARALEGVDELATIRLEARRLEKAEAKLKMEAWQMKLELEAEKLRKE 701
 Oy 375 ARMTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETAASYGVLIWKIRDKRRKOEAVM 434

Db 702 VSRKSEIERKLEQVNTLAEEDDRISRIDRENGELDT-----RIREKMSRK--ASG 750
 Oy 435 GKTLSDLY 441
 Db 751 EEALRLY 757
 RESULT 12
 LMA4_MOUSE STANDARD; PRT; 1816 AA.
 ID LMA4_MOUSE
 AC P97927; P70409; O88785;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin alpha-4 chain precursor.
 GN LAMA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
 RP 940-945.
 RC STRAIN=BALB/C; TISSUE=Endothelial cells;
 RX MEDLINE=97363207; PubMed=9219532;
 RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
 RA Sorokin L.M.;
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
 RT endothelium.";
 RL Eur. J. Biochem. 246:727-735(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97202462; PubMed=9049981;
 RA Liu J., Mayne R.;
 RT "The complete cDNA coding sequence and tissue-specific expression of
 RT the mouse laminin alpha 4 chain.";
 RL Matrix Biol. 15:433-437(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=98010627; PubMed=9346933;
 RA Iivanainen A., Korasmaa J., Sahlborg C., Morita T., Bergmann U.,
 RA Thesleff I., Tryggvason K.;
 RT "Primary structure, developmental expression, and immunolocalization
 RT of the murine laminin alpha4 chain.";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RP SEQUENCE OF 836-1106 FROM N.A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97296337; PubMed=9151674;
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sanes J.R.;
 RT "Type laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5, identification of heterotrimeric
 RT laminins 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RP SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97187457; PubMed=9034910;
 RA Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.;
 RT "Distribution of the ten known laminin chains in the pathways and
 RT targets of developing sensory axons.";
 RL J. Comp. Neurol. 378:547-561(1997).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule

| | | | | | | |
|-----------------------|----------|---|--------------|-------------------------|--------------|----------------|
| FT | CARBOHYD | 333 | 333 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 458 | 458 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 550 | 550 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 571 | 571 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 574 | 574 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 631 | 631 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 639 | 639 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 735 | 735 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 751 | 751 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 754 | 754 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 780 | 780 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 803 | 803 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 1088 | 1088 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 1283 | 1283 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CARBOHYD | 1361 | 1361 | N-LINKED | (GLCNAC. .) | (POTENTIAL. .) |
| FT | CONFLICT | 8 | 8 | C -> S (IN REF. 2). | | |
| FT | CONFLICT | 18 | 18 | C -> Y (IN REF. 2). | | |
| FT | CONFLICT | 248 | 248 | C -> R (IN REF. 3). | | |
| FT | CONFLICT | 297 | 297 | G -> A (IN REF. 3). | | |
| FT | CONFLICT | 431 | 433 | THR -> HPS (IN REF. 2). | | |
| FT | CONFLICT | 679 | 679 | S -> C (IN REF. 3). | | |
| FT | CONFLICT | 703 | 703 | D -> G (IN REF. 2). | | |
| FT | CONFLICT | 706 | 706 | N -> H (IN REF. 2). | | |
| FT | CONFLICT | 728 | 728 | K -> R (IN REF. 2). | | |
| FT | CONFLICT | 730 | 730 | F -> I (IN REF. 2). | | |
| FT | CONFLICT | 779 | 779 | R -> G (IN REF. 1). | | |
| FT | CONFLICT | 810 | 810 | R -> S (IN REF. 3). | | |
| FT | CONFLICT | 865 | 867 | APP -> OT (IN REF. 2). | | |
| FT | CONFLICT | 936 | 936 | K -> E (IN REF. 3). | | |
| FT | CONFLICT | 970 | 970 | L -> V (IN REF. 3). | | |
| FT | CONFLICT | 1132 | 1132 | H -> R (IN REF. 2). | | |
| FT | CONFLICT | 1200 | 1200 | F -> I (IN REF. 2). | | |
| FT | CONFLICT | 1382 | 1382 | D -> A (IN REF. 2). | | |
| FT | CONFLICT | 1413 | 1414 | NS -> EF (IN REF. 1). | | |
| FT | CONFLICT | 1483 | 1489 | A -> S (IN REF. 2). | | |
| SO | SEQUENCE | 1816 AA; | 201818 MM; | B49C45F3A45999D8 CRC64; | | |
| | | | | | | |
| Query Match | | | | | | |
| Best Local Similarity | | 4.9%; | Score 148.5; | DB 1; | Length 1816; | |
| Matches 104; | | Conservative | 75; | Mismatches 214; | Indels 137; | Gaps 24; |
| OY | 2 | ESSKMDSPGALQTNPLKHTDRSAGRPVPEFGGVEKKEKVKVEDKYEKKCHLYLC | 61 | | | |
| Db | 46 | DSEHSIDSGVYTLGRPLPAERCD--Ag-----FRTLSG--ECAPCD--C | 84 | | | |
| OY | 62 | SPKQTEC--GARFCECSMAALLSSSPKTOAESIVDKV-----FRDNC----- | 105 | | | |
| Db | 85 | NNSHSECLDGSGLCHQCR--NTTGEHCEKGLDGYIGDSINGTRPFOPCPRLPHLAN | 141 | | | |
| OY | 106 | ----CKRETLAQIYCRNDSRG-----CAEOLITLHLVH--LKNDCHFEELP-CVRPD | 152 | | | |
| Db | 142 | PAESCYRRNGAARICCKENYVGPNCERCAPGYGNPMLIGSTCKKCDSCGNSDPMILFED | 201 | | | |
| OY | 153 | CKEKYLKRLDRHYEAKCK--YREATCSGKSQYPMIALQKHEDPDCVAVVSC-PHRCS | 209 | | | |
| Db | 202 | C-----DEITGQGRNCLNLTNTGKCEKCAP--GYGDARTAKCAVNCNGGGPCD | 249 | | | |
| OY | 210 | VQTLRSELASHLSECVNAPSTCSFKRYGVFOGTN-----QINAREHSS | 255 | | | |
| Db | 250 | -----SVTGCLEEGFEVPTGCD---KCVMDLTDRLALALSTIEESKGLSVSSGAA | 299 | | | |
| OY | 256 | AVOHYNILKEMSNSEKKEVSILOHNSVEKKNSSIOSLHQOTSFELEIF-----RQK | 306 | | | |
| Db | 300 | AHRHTYTDNKNSTIHLRLTRLSERENOYTLRKIQINNSENFTLSSLPLDVEGLHEKGSQASRK | 359 | | | |
| OY | 307 | EMLRNNES-----KLILQVRYIDSOAEKLEKLEIDREIFRPNWME-----EADSM | 350 | | | |
| Db | 360 | GMIVKEKESMDITIDATHLYEQAHHMRKIQIGINSKMLYIGENQELGPEETAEKLYLAQMK | 419 | | | |
| OY | 351 | KSSVESLQNRVTELESYDKSAGQVARTGTLLESOLSRHD-----QMLSVHDITRLA | 400 | | | |
| Db | 420 | LEETRSPQPLFTHRELYVDEADEAQEILLSONENQORLHNDTRSLFPVYVLQGLDDYNAKLS | 479 | | | |

```

QY 401 DMDLRF-----QVLETSYNGVLIWKIRDYKR-----KROAVMGKTLISL 440
DB 480 DLOESINALDHRVADADNMRAITFRORDHEKQHEKVEKQMEYVGASLGM 529

RESULT 13
ID YD86 SCHPO STANDARD: PRT; 1957 AA.
AC 010411:
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein Clif3.06c in chromosome 1.
GN SPAC1F3.06C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gylliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins K., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Skellion J., Simmonds M., Squares R., Squares S., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymopre B.,
RA Melteni I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mambuti R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: Z70690; CAA94624.1;
KW Hypothetical protein.
SQ SEQUENCE 1957 AA; 22785 MW; 3FA80CA06171D9DA CRC64;

Query Match 4.9%; Score 148; DB 1; Length 1957;
Best Local Similarity 20.3%; Pred. No. 0.26; Indels 174; Gaps 23;
Matches 105; Conservative 83; Mismatches 156;

QY 40 KEKVFVTEDEKYKCEKCHVILCSKQTECGHRCFSCMAALLSSSPCTACQESI----- 95
DB 1416 KESLISLERS-----LSNQROKESLIDAKNELHMDPDSRKNSLMEKTESIN 1466
QY 96 --VKDKVFNCKNCKRETLAQICRNESRGCAEQ-----TLGLHL 134
DB 1467 SSLDDKSFELASVVERKIGALQ-KLHSESLSLMENINSQLOEAKRKIQVDESTIOELDHEI 1525

```

```

QY 135 VILKNDHFELPCVRDCKEYLRKDLRDHYKACKYREATCSHCKSQVPMIALOKHED 194
DB 1526 TASKRN--NYEG-----KINDKDSIIR-DLSNIEQL-----NNLIAEKSVAVKRLSTEKSE 1574
QY 195 -----TDCPCVYVSCPHKCSQVTLT--RSELSAHLSECVNAPSTCSFKRYGCVFGTN 245
DB 1575 ILQFNSRLADLEY-----HKSOVESLGRSKLK-----LASTT 1607
QY 246 OIKRAHE-----ASSAVOHVNLKEMSN-----SLEKKYSLLONESYEKKK 286
DB 1608 EELQIAENERSLITPTBMDLQNOVKDLSNICKDLSSEDLRTLRSLSESVASLQKECKIKSN 1667
QY 287 SIQSLHNDICS-----FELIEIRQKEMLRNNSEKILHFORVDSQAEKLKDEIRP 339
DB 1668 IYESLQDVLTVQARNAELEDEVSRSVDKIRRDREHL-----SGKLKHLHSLQLEE 1720
QY 340 FROMNEADSMKSSVESLQNRVTELESYKSGAGVARNITGLLESQLSRHDQMLSYHDRL 359
DB 1721 QHETFFRAE-----QQRMTOL-----GFLKETVYKOEKRLKKNLRLQ 1757
QY 400 ADMDLRFQVLETSYNGVLIWKIRDYKR-----KROAVMGKTLISLXSOEYGYGYKKA 456
DB 1758 EQLIPRSSILYVESY-----IRDIKEIIVLOERLNGIEL-----SQQLPKGYFGY----- 1803
QY 457 RYVLNDDGKMGKTHLSLFEVIRGEXYDALLPWPFQKV 494
DB 1804 -----FKTRNREMEVL--DSFRQOV 1822

RESULT 14
ID GCG4 HUMAN STANDARD: PRT; 2230 AA.
AC Q13439; Q14436; Q13270; Q13654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Golgi autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa
DE golgin) (Golgin-245) (72.1 protein).
GN GOLG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=96215236; PubMed=8626529;
RA Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.;
RT "Molecular characterization of trans-Golgi p230: a human peripheral
RT membrane protein encoded by a gene on chromosome 6p12-22 contains
RT extensive coiled-coil alpha-helical domains and a granin motif."
RL J. Biol. Chem. 271:8328-8337(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Seeliger H.P.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 131-2230 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=96125112; PubMed=8537393;
RA Fritzel M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.;
RT "Molecular characterization of golgin-245, a novel Golgi complex
RT protein containing a granin signature."
RL J. Biol. Chem. 270:31262-31268(1995).
RN [4]
RP SEQUENCE OF 524-672 FROM N.A.
RC TISSUE=Gastric fundus;
RA Balague C.;
RL Thesis (1994), Instituto municipal de Investigacion medica, Spain.
CC -!- FUNCTION: MAY PLAY A ROLE IN VESICULAR TRANSPORT FROM THE TRANS-
CC GOLGI
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE
CC GOLGI MEMBRANE.

```


FT CONFLICT 135 135 H -> Q (IN REF. 1).
FT CONFLICT 185 185 T -> R (IN REF. 1).
SQ SEQUENCE 1102 AA: 128008 MM: 2293668D049825DC CRC64:

Query Match 4.9%: Score 146; DB 1; length 1102;
Best Local Similarity 21.4%: Pred. No. 0.17;
Matches 85; Conservative 69; Mismatches 143; Indels 100; Gaps 17;

QY 96 VKDVFVFNCKCKREI-LALQIYCNESRGCADLTGLHLVHLKNDCHFEELPCVRPDC 154
DB 695 VKKQVEDE--KSEVQLALE-----EAGALEHESKTLRFQL-----ELSQLKADFE 739
QY 155 EKVLRKD-----LKDHYEKACKYREATC-SHCKSQVPMIALQKHEDTDCPCVYVSCPH-- 206
DB 740 RKLAEKDEMONIRRNQRTIDSLQSTLDSFARSRSNEAIRLKKMEGDLNEMETQLSHAN 799
QY 207 -----KCSVOTLRSLELS-----AHLSECVNAPSTCSFRRYGCVFQGTNOQIKA- 250
DB 800 RHAAEATKSARGLOTOTK-ELQVOLDLGLHNEDLKEQLAVSDRRNN-LIQSELDLRLAL 857
QY 251 -----HEASSAVQHVNLKESWSNS-----LEKKVSLQNESVEKNKSIQSL 291
DB 858 LDQTEBARAKLAHEHLEATERVNLHTQNTSLINQKKLEGDISQMONVEVESIQECRNA 917
QY 292 HNOICSEIEIERQKEMLRNNESKILHQRVIDSOAEKELDKKEIRPFRQNMEEADSM- 350
DB 918 EOKAKKAITDAMMAEELKKEODTSAHLERNKKMNEQITKDQKRL-----DEAEQIA 970
QY 351 ----KSSVESLQNRVTELES-----VKSAGQVARNGTGLLESQLSRHDQMLSVH 395
DB 971 LKGGKKQIQKLESVRLELENLEENLRNSDAQGARKFERRIKELTYQSEDEKKNLA-- 1028
QY 396 DIRLADMQLRFQVLEFASNGVLWIKIRYKRRKQEA 432
DB 1029 --RMQDLIDKIQQL-----KVKSYKHOAEAA 1051

Search completed: December 19, 2002, 14:54:48
Job time : 19 secs

